a sequence tagged site (STS), which is defined by a pair of primers, specific to a particular microsatellite sequence, each primer having an average length of 20 ± 3 bases and flanking the particular microsatellite sequence,

E1 cont

wherein each of said microsatellite markers is formed by amplification of the microsatellite sequence by a polymerase chain reaction, to form markers of different length, wherein the primer pairs are selected from at least one of the pairs SEQ ID NO. x and SEQ ID NO. $x + 1$, where x = odd numbers from 1 through 465.

E2

3. (three times amended) The set of claim 1, wherein the microsatellite sequence <u>of at least one of said markers of said set</u> is a composite microsatellite sequence <u>comprising at least two microsatellite sequences</u>.

4. (three times amended) The set of claim 1, wherein the microsatellite sequence <u>of at least one marker of said set</u> is an imperfect sequence, in which individual bases are mutated <u>within said sequence</u>.

E3

7. (three times amended) The method of claim 6, wherein a gel chosen from the group consisting of [highly resolving]

agarose gels, native polyacrylamide gels and denaturing polyacrylamide gels [are] is used for the separating step.

11. (amended) The set of claim 1, comprising 233 markers defined by 233 primer pairs, which primer pairs are defined as all primer pairs SEQ ID NO. x and SEQ ID NO. x+1, where x=odd numbers from 1 through 465 [wherein the pairs of primers comprise all of the 233 primer pairs].

Please add the following new claims:

12. The set of claim 3, wherein the composite microsatellite sequence is of the formula $(GA)_n(AT)_m$.

13. The set of claim 4, wherein the imperfect microsatellite sequence is of the formula $(GA)_n(CA)(GA)_m$.

REMARKS

This is in response to the official action mailed on February 25, 2000. Reconsideration in view of the following is respectfully considered.